

## 井川

## SEQUENCE LISTING

<110> YU, LEI <120> MU OPIOID RECEPTOR: COMPOSITIONS AND METHODS <130> INDA:002USD1 <140> 09/841,720 <141> 2001-04-24 <150> 08/120,601 <151> 1993-09-13 <160> 9 <170> PatentIn Ver. 2.1 <210> 1 <211> 1618 <212> DNA <213> RAT <220> <221> CDS <222> (214)..(1407) <400> 1 cqtqqaaqqq qqctacaaqc aqaqqaqaat atcaqacgct cagacgttcc cttctgcctg 60 ccgctcttct ctggttccac tagggctggt ccatgtaaga atctgacgga gcctagggca 120 gctgtgagag gaagaggctg gggcgcgtgg aacccgaaaa gtctgagtgc tctcagttac 180 agectaceta gteegeagea ggeetteage ace atg gae age age ace gge eca 234 Met Asp Ser Ser Thr Gly Pro 1 ggg aac acc agc gac tgc tca gac ccc tta gct cag gca agt tgc tcc 282 Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser cca gca cct ggc tcc tgg ctc aac ttg tcc cac gtt gat ggc aac cag 330 Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln 25 30 tee gat eea tge ggt etg aac ege ace ggg ett gge ggg aac gae age 378 Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser 40 45

ctg tgc cct cag acc ggc agc cct tcc atg gtc aca gcc att acc atc Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile

60

70

B

atg g Met A														474
ctg g Leu V														522
aac a Asn I 1							_	_	_	_	_		_	570
aca c Thr L 120	_			_	-	-								618
gga a Gly T														666
ttc a Phe T		-												714
gct g Ala V	al (	_			_		-	_	_		_			762
gcc a Ala L 1			_		_	_								810
ctg c Leu P 200														858
gat t Asp C	_			_								 	_	906
ctc a Leu L			_	_				-			_			954
atc a Ile T	hr V		_			-	-							1002
atg c Met L 2														1050
cgg a Arg M														1098

By.

280 · 285 290	295									
atc cac atc tac gtc atc atc aaa gcg ctg atc acg a  Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr I  300 305										
aca ttt cag acc gtt tcc tgg cac ttc tgc att gct t Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala I 315 320										
aac agc tgc ctg aat cca gtt ctt tac gcc ttc ctg g Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu A 330 335										
aag cga tgc ttc aga gag ttc tgc atc cca acc tcg t Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser S 345 350 355										
cag caa aac tcc act cga gtc cgt cag aac act agg g Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg C 360 365 370										
acg gct aat aca gtg gat cga act aac cac cag cta g Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu C 380 385										
gca gaa act gct cca ttg ccc taactgggtc tcacaccatc Ala Glu Thr Ala Pro Leu Pro 395	c cagaccctcg 1437									
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Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly I	Leu Asn Arg Thr 45									

Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser 50 · 55 60

Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val 65 70 75 80

Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr 85 90 95

Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu 100 105 110

Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr 115 120 125

Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile 130 135 140

Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr 145 150 155 160

Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu 165 170 175

Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp 180 185 190

Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr 195 200 205

Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro 210 215 220

Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala 225 230 235 240

Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile 245 250 255

Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp 260 265 270

Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val 275 280 285

Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala 290 295 300

Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe 305 310 315 320

Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr 325 330 335

Brt

Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln 360 Asn Thr Arq Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn 375 380 370 His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro 390 395 <210> 3 <211> 1618 <212> DNA <213> RAT <220> <221> CDS <222> (339) .. (1232) <400> 3 cgtggaaggg ggctacaagc agaggagaat atcagacgct cagacgttcc cttctgcctg 60 ccgctcttct ctggttccac tagggctggt ccatgtaaga atctgacgga gcctagggca 120 gctgtgagag gaagaggctg gggcgcgtgg aacccgaaaa gtctgagtgc tctcagttac 180 agectaceta georgeagea ggeetteage accatggaca geageacegg cecagggaac 240 accagegact geteagacec ettageteag geaagttget eeceageace tggeteetgg 300 ctcaacttgt cccacgttga tggcaaccag tccgatcc atg cgg tct gaa ccg cac 356 Met Arg Ser Glu Pro His 5 1 cgg get tgg cgg gaa cga cag cct gtg ccc tca gac cgg cag ccc ttc 404 Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro Phe 10 15 cat ggt cac age cat tac cat cat ggc cct cta ctc tat cgt gtg tgt His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val Cys agt ggg cct ctt cgg aaa ctt cct ggt cat gta tgt gat tgt aag ata 500 Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys Ile 40 45 cac caa aat gaa gac tgc cac caa cat cta cat ttt caa cct tgc tct His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys Ser

70

Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile



55

ggc a Gly A	_	_		-	-	-			_				-			596
cct g Pro A	-			_	_						_		_	_	_	644
ctc a Leu A		_					_		_							692
cat g His G 1		_		_			_									740
gga t Gly P 135		-			_		_									788
gat c Asp P				_				_	_		_					836
aaa a Lys I		_	_		_		_	_				_				884
aac c Asn L	_	_			_					_	_					932
ttt c Phe H 2			_	_					_							980
ctt a Leu T 215	_				_	_		_					_			1028
cag g Gln G																1076
att t Ile T		_	_	_	_						_				-	1124
gct g Ala A	-		_		_					_	_					1172
ctg c Leu H		_					-									1220

Blant

280 . 285 . 290

cgc ctt cct gga tgaaaacttc aagcgatgct tcagagagtt ctgcatccca 1272 Arg Leu Pro Gly 295

acctegteca egategaaca geaaaactee actegagtee gteagaacae tagggaacat 1332 ceetecaegg etaatacagt ggategaact aaccaecage tagaaaatet ggaggeagaa 1392 actgetecat tgeeetaact gggteteaea eeateeagae eetegetaag ettagaggee 1452 geeatetaeg tggaateagg ttgetgteag ggtgtgtggg aggetetggt tteetgagaa 1512 accatetgat eetgeattea aagteattee tetetggeta etteaetetg eacatgagag 1572 atgeteagae tgateaagae eagaagaaag aagagaetae eggaea 1618

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Leu Leu Tyr Arg Val Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His
35 40 45

Val Cys Asp Cys Lys Ile His Gln Asn Glu Asp Cys His Gln His Leu
50 55 60

His Phe Gln Pro Cys Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala 65 70 75 80

Leu Ser Glu Cys Gln Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His
85 90 95

Pro Leu Gln Asp Arg Asp Leu Asn Arg Leu Leu Gln His Val His Gln
100 105 110

His Ile His Pro Leu His His Glu Arg Gly Pro Leu His Cys Cys Leu 115 120 125

Pro Pro Ser Gln Ser Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn 130 135 140

Arg Gln Arg Leu Gln Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys 145 150 155 160

B1

Asn Val His Gly Asn His Lys Ile Gln Ala Gly Val His Arg Leu His 165 170 175												
Pro His Val Leu Pro Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn 180 185 190												
Leu Cys Leu Tyr Leu Arg Phe His His Ala Asp Pro His His Cys 195 200 205												
Val Leu Arg Pro Asp Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile 210 215 220												
Gly Leu Gln Arg Lys Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly 225 230 235 240												
Ala Gly Gly Arg Gly Cys Ile Tyr Arg Leu Leu Asp Pro His Pro His 245 250 255												
Leu Arg His His Gln Ser Ala Asp His Asp Ser Arg Asn His Ile Ser 260 265 270												
Asp Arg Phe Leu Ala Leu Leu His Cys Phe Gly Leu His Glu Gln Leu 275 280 285												
Pro Glu Ser Ser Leu Arg Leu Pro Gly 290 295												
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By

<400> 7

Met Glu Leu Val Pro Ser Ala Arg Ala Glu Leu Gln Ser Ser Pro Leu

1 . 5 10 15

Val Asn Leu Ser Asp Ala Phe Pro Ser Ala Phe Pro Ser Ala Gly Ala 20 25 30

Asn Ala Leu Gly Ser Pro Gly Ala Arg Ser Ala Ser Met Leu Ala Leu 35 40 45

Ala Ile Ala Ile Thr Ala Leu Tyr Ser Ala Val Cys Ala Val Gly Leu 50 55 60

Leu Gly Asn Val Leu Val Met Phe Gly Ile Val Arg Tyr Thr Lys Leu 65 70 75 80

Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala 85 90 95

Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr Leu Met Glu
100 105 110

Thr Trp Pro Phe Gly Glu Leu Leu Cys Lys Ala Val Leu Ser Ile Asp 115 120 125

Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Thr Met Met Ser Val 130 135 140

Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg 145 150 155 160

Thr Pro Ala Lys Ala Lys Leu Ile Asn Ile Cys Ile Trp Val Leu Ala 165 170 175

Ser Gly Val Gly Val Pro Ile Met Val Met Ala Val Thr Gln Pro Arg 180 185 190

Asp Gly Ala Val Val Cys Met Leu Gln Phe Pro Ser Pro Ser Trp Tyr 195 200 205

Trp Asp Thr Val Thr Lys Ile Cys Val Phe Ile Phe Ala Phe Val Val 210 215 220

Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Leu Leu Arg Leu 225 230 235 240

Arg Ser Val Arg Leu Leu Ser Gly Ser Lys Glu Lys Asp Arg Ser Leu 245 250 255

Arg Arg Ile Thr Arg Met Val Leu Val Val Val Gly Ala Phe Val Val 260 265 270

Cys Trp Ala Pro Ile His Ile Phe Val Ile Val Trp Thr Leu Val Asp 275 280 285

Bht Cont

Ile Asn Arg Arg Asp Pro Leu Val Val Ala Ala Leu His Leu Cys Ile 295 290

Ala Leu Gly Tyr Ala Asn Ser Ser Leu Asn Pro Val Leu Tyr Ala Phe 315

Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Gln Leu Cys Arg Thr Pro 330

Cys Gly Arg Gln Glu Pro Gly Ser Leu Arg Arg Pro Arg Gln Ala Thr 340

Thr Arg Glu Arg Val Thr Ala Cys Thr Pro Ser Asp Gly Pro Gly Gly 360

Gly Ala Ala Ala 370

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Ser Pro Gly Gly Cys Gly Glu Gly Leu Cys Ser Arg Gly Pro Gly Ser

Gly Ala Ala Asp Gly Met Glu Glu Pro Gly Arg Asn Leu Ser Gln Asn

Gly Thr Leu Ser Glu Gly Gln Gly Ser Ala Ile Leu Ile Ser Phe Ile

Tyr Ser Val Val Cys Leu Val Gly Leu Cys Gly Asn Ser Met Val Ile

Tyr Val Ile Leu Arg Tyr Ala Lys Met Lys Thr Ala Thr Asn Ile Tyr

Ile Leu Asn Leu Ala Ile Ala Asp Glu Leu Leu Met Leu Ser Val Pro 105

Phe Leu Val Thr Ser Thr Leu Leu Arg His Trp Pro Phe Gly Ala Leu 120

Leu Cys Arg Leu Val Leu Ser Val Asp Ala Tyr Asn Met Phe Thr Ser 135 130

Ile Tyr Cys Leu Thr Val Leu Ser Val Asp Arg Tyr Val Ala Val Val 155 150 145

His Pro Ile Lys Ala Ala Arg Tyr Arg Arg Pro Thr Val Ala Lys Val 165 170 175

Val Asn Leu Gly Val Trp Val Leu Ser Leu Leu Val Ile Leu Pro Ile 180 185 190

Val Val Phe Ser Arg Thr Ala Ala Asn Ser Asp Gly Thr Val Ala Cys 195 200 205

Asn Met Leu Met Pro Glu Pro Ala Gln Arg Trp Leu Val Gly Phe Val 210 215 220

Leu Tyr Thr Phe Leu Met Gly Phe Leu Leu Pro Val Gly Ala Ile Cys 225 230 235 240

Leu Cys Tyr Val Leu Ile Ile Ala Lys Met Arg Met Val Ala Leu Lys
245 250 255

Ala Gly Trp Gln Gln Arg Lys Arg Ser Glu Arg Lys Ile Thr Leu Met 260 265 270

Val Met Met Val Val Met Val Phe Val Ile Cys Trp Met Pro Phe Tyr 275 280 285

Val Val Gln Leu Val Asn Val Phe Ala Glu Gln Asp Asp Ala Thr Val 290 295 300

Ser Gln Leu Ser Val Ile Leu Gly Tyr Ala Asn Ser Cys Ala Asn Pro 305 310 315 320

Ile Leu Tyr Gly Phe Leu Ser Asp Asn Phe Lys Arg Ser Phe Gln Arg 325 330 335

Ile Leu Cys Leu Ser Trp Met Asp Asn Ala Ala Glu Glu Pro Val Asp 340 345 350

Tyr Tyr Ala Thr Ala Leu Lys Ser Arg Ala Tyr Ser Val Glu Asp Phe 355 360 365

Gln Pro Glu Asn Leu Glu Ser Gly Gly Val Phe Arg Asn Gly Thr Cys 370 375 380

Ala Ser Arg Ile Ser Thr Leu 385 390

<210> 9

<211> 369

<212> PRT

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Met Glu Leu Thr Ser Glu Gln Phe Asn Gly Ser Gln Val Trp Ile Pro

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Gln Thr Glu Pro Tyr Tyr Asp Met Thr Ser Asn Ala Val Leu Thr Phe 35 40 45

Ile Tyr Phe Val Val Cys Val Val Gly Leu Cys Gly Asn Thr Leu Val 50 55 60

Ile Tyr Val Ile Leu Arg Tyr Ala Lys Met Lys Thr Ile Thr Asn Ile 65 70 75 80

Tyr Ile Leu Asn Leu Ala Ile Ala Asp Glu Leu Phe Met Leu Gly Leu 85 90 95

Pro Phe Leu Ala Met Gln Val Ala Leu Val His Trp Pro Phe Gly Lys
100 105 110

Ala Ile Cys Arg Val Val Met Thr Val Asp Gly Ile Asn Gln Phe Thr 115 120 125

Ser Ile Phe Cys Leu Thr Val Met Ser Ile Asp Arg Tyr Leu Ala Val 130 135 140

Val His Pro Ile Lys Ser Ala Lys Trp Arg Arg Pro Arg Thr Ala Lys 145 150 155 160

Met Ile Asn Val Ala Val Trp Gly Val Ser Leu Leu Val Ile Leu Pro 165 170 175

Ile Met Ile Tyr Ala Gly Leu Arg Ser Asn Gln Trp Gly Arg Ser Ser 180 185 190

Cys Thr Ile Asn Trp Pro Gly Glu Ser Gly Ala Trp Tyr Thr Gly Phe 195 200 205

Ile Ile Tyr Ala Phe Ile Leu Gly Phe Leu Val Pro Leu Thr Ile Ile 210 215 220

Cys Leu Cys Tyr Leu Arg Ile Ile Ile Lys Val Lys Ser Ser Gly Ile 225 230 235 240

Arg Val Gly Ser Ser Lys Arg Lys Lys Ser Glu Lys Lys Val Thr Arg 245 250 255

Met Val Ser Ile Val Val Ala Val Phe Ile Phe Cys Trp Leu Pro Phe 260 265 270

Tyr Ile Phe Asn Val Ser Ser Val Ser Val Ala Ile Ser Pro Thr Pro 275 280 285

Ala Leu Lys Gly Met Phe Asp Phe Val Val Ile Leu Thr Tyr Ala Asn

B' Cont

290 ~ 295 300

Ser Cys Ala Asn Pro Ile Leu Tyr Ala Phe Leu Ser Asp Asn Phe Lys 305 310 315 320

Lys Ser Phe Gln Asn Val Leu Cys Leu Val Lys Val Ser Gly Ala Glu 325 330 335

Asp Gly Glu Arg Ser Asp Ser Lys Gln Asp Lys Ser Arg Leu Asn Glu 340 345 350

Thr Thr Glu Thr Gln Arg Thr Leu Leu Asn Gly Asp Leu Gln Thr Ser 355 360 365

Ile